

CLAIMS

1. A method of comparing spectral data or like data, which method comprises defining as a group, a
5 plurality of data points within a range of data points for a data item, converting said group of data points to at least one kernel function, assembling the resultant plurality of kernel functions covering all the data points for the data item into a cluster, and
10 projecting said cluster of kernel functions in high dimensional space using Cover's Theorem to define a single searchable reference point for all the data points for said data item, and comparing the said single searchable point for a sample item with the
15 single searchable point for similarly processed comparison items.
2. A method as claimed in claim 1 characterised in that at least one of the groups of data points is
20 converted into a plurality of kernel functions.
3. A method as claimed in claim 2 wherein the single searchable reference point is defined by a vector function.

4. A method as claimed in claim 1 wherein variables
in data points within an item define a radial basis
function for the said single searchable point which
constitute a measure of the spread of said variables
5 for that item about a mean.

5. A method as claimed in claim 1 wherein
uncertainty in the comparison of points is resolved
using transformations in possibility theory.

10 6. A method as claimed in claim 1 wherein the data
points are selected across a range of data, in which
the data is normalized by comparing all the data
magnitudes as a proportion of the highest, which is
15 rated at 1.

7. A method as claimed in claim 1 wherein the data
is spectral data.

20 8. An apparatus for screening of microorganisms
characterised by spectroscopic means for producing
spectral data of the sample organism database means
containing spectral data for a range of microorganisms
and comparison means for comparing the spectral data
25 of the sample with that of the database to permit

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classification/identification of the sample,
characterized in that the spectroscopic means
comprises means for producing spectral data of the
sample organism by MALDI-TOF techniques and in that
5 the database contains MALDI-TOF-MS spectral data, and
in that the comparison means is a method as claimed in
claim 1.

9. Apparatus as claimed in claim 8 wherein the
10 spectral data in the database is arranged in groups of
data according to the genus of each microorganism with
sub-divisions corresponding to each strain of
microorganism.

10. Apparatus as claimed in claim 8 characterised in
that the sample of unidentified microorganism is
prepared by a technique selected from the group
consisting of (i) taking cells from a culture and
applying them to a sample plate comprising a matrix
20 and (ii) by admixing the cells with the matrix prior
to subjecting to MALDI-TOF-MS analysis in order to
retain the cellular integrity of the sample.

11. Apparatus as claimed in claim 6 characterised by
25 means for bombarding a sample matrix mixture with

laser energy to create a gas phase ionic species which is then pulsed into a flight conduit or tube for identification of both positive and/or negative ions.